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**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869B**

DATE: 03/26/2002
TIME: 21:16:41

INPUT SET: S36811.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.

10 (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
11 Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 35

15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Rop
17 (B) STREET: One In
18 (C) CITY: Boston
19 (D) STATE: MA
20 (E) COUNTRY: USA
21 (F) ZIP: 02110

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869

(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/893,274
 (B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/306,511
 (B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/248,812
 (B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

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47      (A) APPLICATION NUMBER: US 08/227,371
48      (B) FILING DATE: 14-APR-1994
49
50      (vii) PRIOR APPLICATION DATA:
51          (A) APPLICATION NUMBER: US 08/154,915
52          (B) FILING DATE: 18-NOV-1993
53
54      (vii) PRIOR APPLICATION DATA:
55          (A) APPLICATION NUMBER: US 07/991,997
56          (B) FILING DATE: 17-DEC-1992
57
58      (viii) ATTORNEY/AGENT INFORMATION:
59          (A) NAME: Vincent, Matthew P.
60          (B) REGISTRATION NUMBER: 36,709
61          (C) REFERENCE/DOCKET NUMBER: GPCI-P10-071
62
63      (ix) TELECOMMUNICATION INFORMATION:
64          (A) TELEPHONE: (617) 951-7739
65          (B) TELEFAX: (617) 951-7050
66
67
68      (2) INFORMATION FOR SEQ ID NO:1:
69          (i) SEQUENCE CHARACTERISTICS:
70              (A) LENGTH: 994 base pairs
71              (B) TYPE: nucleic acid
72              (C) STRANDEDNESS: both
73              (D) TOPOLOGY: linear
74
75          (ii) MOLECULE TYPE: cDNA
76          (ix) FEATURE:
77              (A) NAME/KEY: CDS
78              (B) LOCATION: 41..508
79
80      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
81
82      CGGAGAGGGG GAGAACAGAC AACGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG      55
83                               Met Asp Pro Ala Ala
84                               1           5
85      GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC      103
86      Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala
87                               10          15          20
88      CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG      151
89      Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu
90                               25          30          35
91      CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG      199
92      Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met
93                               40          45          50
94      ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTC CAC GGC GCG GAG      247
95      Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu
96                               55          60          65
97      CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT      295
98      Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala
99                               70          75          80          85

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100	GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343
101	Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly	
102	90 95 100	
103	GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391
104	Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu	
105	105 110 115	
106	GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439
107	Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala	
108	120 125 130	
109	GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487
110	Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu	
111	135 140 145	
112	GGT CCC TCA GAC ATC CCC GAT TGAAAGAACCG AGAGAGGCTC TGAGAACCT	538
113	Gly Pro Ser Asp Ile Pro Asp	
114	150 155	
115	CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACTGC CCCCCGCCACA	598
116	ACCCACCCCG CTTTCGTAGT TTTCATTAG AAAATAGAGC TTTTAAAAAT GTCCCTGCCTT	658
117	TAAACGTAGA TATAAGCCCTT CCCCCACTAC CGTAAATGTC CATTATATC ATTTTTTATA	718
118	TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTCACT GTGTTGGAGT	778
119	TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTATG TGGGCATTTC TTGCGAGCCT	838
120	CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTGT GTGAACCTAGG GAAGCTCAGG	898
121	GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA	958
122	AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA	994

123
124 (2) INFORMATION FOR SEQ ID NO:2:

125
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 156 amino acids
128 (B) TYPE: amino acid
129 (D) TOPOLOGY: linear

130
131 (ii) MOLECULE TYPE: protein

132
133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

134	Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu	
135	1 5 10 15	
136	Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu	
137	20 25 30	
138	Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro	
139	35 40 45	
140	Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu	
141	50 55 60	
142	Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg	
143	65 70 75 80	
144	Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val	
145	85 90 95	
146	Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg	
147	100 105 110	
148	Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg	
149	115 120 125	
150	Tyr Leu Arg Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg	
151	130 135 140	

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153	Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp		
154	145	150	155
155			
156	(2) INFORMATION FOR SEQ ID NO:3:		
157			
158	(i) SEQUENCE CHARACTERISTICS:		
159	(A) LENGTH: 837 base pairs		
160	(B) TYPE: nucleic acid		
161	(C) STRANDEDNESS: single		
162	(D) TOPOLOGY: linear		
163	(ii) MOLECULE TYPE: cDNA		
164			
165	(ix) FEATURE:		
166	(A) NAME/KEY: CDS		
167	(B) LOCATION: 328..738		
168			
169	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:		
170			
171	GAGGACTCCG CGACGGTCCG CACCCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCGG	60	
172	CGCTAGGCGC TTTTCCCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGGCCAGGA	120	
173	AAAGCCCCGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCCAACGC CGCAGAACAA	180	
174	GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCTTA GGAAGGAGAG AGTGCGCCGG	240	
175	AGCAGCGTGG GAAAGAAGGG AAGAGTGTG TTAAGTTAC GGCCAACGGT GGATTATCCG	300	
176	GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG	351	
177	Met Arg Glu Glu Asn Lys Gly Met		
178	1 5		
179	CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA	399	
180	Pro Ser Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly		
181	10 15 20		
182	CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC	447	
183	Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn		
184	25 30 35 40		
185	GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC	495	
186	Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly		
187	45 50 55		
188	AGC GCC CGC GTG GCG GAG CTG CTG CTC CAC GGC GCG GAG CCC AAC	543	
189	Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn		
190	60 65 70		
191	TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCT CGG	591	
192	Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg		
193	75 80 85		
194	GAG GGC TTC CTG GAC ACG CTG GTG CTG CAC CGG GCC GGG GCG CGG	639	
195	Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg		
196	90 95 100		
197	CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG	687	
198	Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu		
199	105 110 115 120		
200	GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG	735	
201	Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly		
202	125 130 135		
203	GAC TGACGCCAGG TTCCCCAGCC GCCCACAAAGC ACTTTATTTT CTTACCCAAT	788	
204	Asp		
205			

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206 TTCCCACCCC CACCCACCTA ATTGATGAA GGCTGCCAAC GGGGAGCGG

207

208 (2) INFORMATION FOR SEQ ID NO:4:

209

210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 137 amino acids
212 (B) TYPE: amino acid
213 (D) TOPOLOGY: linear

214

215 (ii) MOLECULE TYPE: protein

216

217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

218

219 Met	Arg	Glu	Glu	Asn	Lys	Gly	Met	Pro	Ser	Gly	Gly	Ser	Asp	Glu	
220 1					5				10				15		
221 Gly	Leu	Ala	Thr	Pro	Ala	Arg	Gly	Leu	Val	Glu	Lys	Val	Arg	His	Ser
222								20		25			30		
223 Trp	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Gly	Val	Asn	Arg	Phe	Gly	Arg	Arg
224								35		40		45			
225 Ala	Ile	Gln	Val	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu
226							50		55		60				
227 Leu	Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr
228							65		70		75		80		
229 Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val
230							85		90		95				
231 Val	Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly
232							100		105		110				
233 Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Arg	Gly	His	Arg	Asp	Val	Ala
234							115		120		125				
235 Gly	Tyr	Leu	Arg	Thr	Ala	Thr	Gly	Asp							
236							130		135						

237

238 (2) INFORMATION FOR SEQ ID NO:5:

239

240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 853 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: both
244 (D) TOPOLOGY: linear

245

246 (ii) MOLECULE TYPE: cDNA

247

248 (ix) FEATURE:
249 (A) NAME/KEY: CDS
250 (B) LOCATION: 213..587

251

252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

253

254 GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC 60

255

256 GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG 120

257

258 GACAGCGAGC TGCGCTCTGG CTTTCTGAA CATGTTGTG AGGCTAGAGA GGATCTTGAG 180

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**SEQUENCE VERIFICATION REPORT
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